Please replace the paragraph beginning at page 25, line 18 of the specification with the following rewritten paragraph:

-- Figures 42a and 42b show the ESI-MS of a 27-mer RNA/DNA hybrid target in the presence of paromomycin alone (panel a), and in the presence of both paromomycin and a combinatorial library (panel b). --

Please replace the paragraph beginning at page 154, line 15 of the specification with the following rewritten paragraph:

-- Cleavage and fragmentation of the complex by CID afforded information regarding the location of binding of the paromomycin to the chimeric nucleic acid. CID was found to produce no fragmentation at the dA sites in the nucleic acid. Thus paromomycin must bind at or near all three dA residues. Paromomycin therefore is believed to bind to the dA bulge in this RNA/DNA chimeric target, and induces a conformational change that protects all three dA residues from being cleaved during mass spectrometry. See Figures 41a and 41b. --

Please replace the paragraph beginning at page ~~15~~ 155, line 18 of the specification with the following rewritten paragraph:

-- The ESI mass spectrum so obtained, shown in Figures 42a and 42b, demonstrated the presence of new signals for the (M-5H)5- ions at m/z values of 1897.8, 1891.3 and 1884.4. Comparing these new signals to the ion peak for the 27-mer alone the observed values of m/z of those members of the combinatorial library that are binding to the target can be calculated. The masses of the binding members of the library were determined to be 566.5, 534.5 and 482.5, respectively. Knowing the structure of the scaffold, and substituents used in the generation of this library, it was possible to determine what substitution pattern (combination of substituents) was present in the binding molecules. --

In the Claims:

Amend claims 19, 21, 26, 31, 32, and 34 to read as follows.